Serial No.: To Be Assigned

54 AGC	108 GCT A	162 AAT N	216 GCT A	270 GCC A	324 GGA G	378 CTT L
GAA	GAA E	AGA R	GCA A	GAG E	GCT	GTC V
ACT	GGA		GCA	GTG V	CTG L	AAA K
45 TAA	99 CTT L	153 GGA G	207 GCT A	261 AGT S	315 CAG Q	369 AAC N
36 TTT GCT TGT	GGT G	GGA G	GAG	ACC	ACA T	CTC L
GCT	CGA R	GAA E	AGT S	TTC F	$ ext{rTr}$	ATT I
36 TYT	90 GAT D	144 AGA ( R	198 ATC I	252 CAT H	306 CAA Q	360 AAT N
GCC GCA	GCA	AGA R	TYT	CAG Q	CAA Q	ATG M
	GGA G	CAG Q	AAT N	CAG Q	CGG R	CTG L
27 GCT	81 GAA E		189 GTG V		297 TTT F	351 GAT D
ATT		GGT	ATT I	CCC		
AAG	CTA L	GGA G	GGA G	CCT		GCC
18 TCT ?	72 GCT A	126 GGA G	180 GGA G	234 CCG P	288 GTT V	342 GGT G
ATC	AAG K	TYTT F	GTT V	GAA E	GAA E	GTG V
ACC	GCA A	CTC L	ATA I	CCA P	GAG E	GAG E
9 CAT	63 CTT L	117 GGC G	171 GGG G	225 ACT T	279 AGT S	333 ATG M
TYT	TYYY	GGA G	GGA G	TAT Y	GAA E	GAC D
9 5' TTT TTT CAT	63 ATG TTT CTT M F L	CTT GGA (	ATT GGA	CAG TAT	TCA GAA	333 CCA GAC ATG P D M
5 .			:			

### FIGUREIA

432 AGC S	486 TTT F	540 GAC D	94 CC	648 GCT A	02 IG	756 ATT I
CGG	GAA	TAT	CAG	TAT	CGC	CTG
R	E	Y	Q	Y	R	L
TGC	GAA	CAG	CTG	CGG	GTC	
	E	Q	L	R	V	0
423	477	531	585	639	693	747
ACC	TTT	AAG	GCT	CGC	TTG	GAT
T	F	K	A	R	L	D
GAC D		TAT Y				
CTT	CTG L	GTT V	CGG R	ATT I	AGC	GAT D
	468 AAG K					
T'I'T F	GGT	CAG Q	CAG Q	CAA Q	TTC	GAT D
GGT G	ACT T	TGG W	TCT	$\frac{\texttt{TAC}}{\texttt{Y}}$	AAT N	CTG L
405	459	513	567	621	675	729
GAC	ACG	AAA	AGT	CTT	AAC	TCT
D	T	K	S	L	N	S
	GAC	AAG	GGA	CAA	TTT	AAG
	D	K	G	Q	F	K
AAG	AGT	ATC	CTG	GAA	GAT	$ ext{TTC}$
K	S	I	L	E	D	
396	450	504	558	612	666	720
CTT	GAC	AAC	TCT	AAT	ATG	GCC
L	D	N	S	N	M	A
GAT	ATG	AAC	9	CTA	GAT	CGT
D	M	N	9	L	D	R
AAA	GTC	TGG	TCT	CAG	GGA	TTT
K	V	W		Q	G	F
387 CAC H	441 TCT (	495 CTG L	549 CAT H	603 TTC F	657 GAT D	711 ATG M
AAG	GTG	TAT	GAC		GAA	GCC
K	V	Y	D	199	E	
TCT	ATT	AAG K	AGG R	GCA	AAT N	GAT GCC D A

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864 GTA	918 CAC	972 GAT	
		ACA	
		AAA	
855 TGC	909 AAG	963 ATT	
	ე99	TGA	
AAA		TGC	
846 TGA	900 TTT	954 TAC	
GAC			_
		၁၁၅	981 CGA AAA AAA AAA AAA AAA A 3'
837 GGA		945 GCT	999 AAA
GGA			AAA
		TCA	AÄA
		936 TGA	990 AAA
ATC	TAC	TTC	AAA
AAG		TAT	AAA
	873 TGC	927 ACA	981 CGA
GAA			ATT TCA
TGA	CAC	AAC	ATT
	AAG ATC CTC CCT GGA GGA CAG GAC TGA AAA CCT TGC CAA GCT	819         828         837         846         855           GAA GTC AAG ATC CTC CCT GGA GGA CAG GAC TGA AAA CCT TGC CAA GCT         TGC CAA GCT         TGC TGA TAC CCT GTG CAA CAG CTC TCA TTT CCT GGC AAG CTC TTT	GAA         GTC         AAG         ATC         CTC         CCT         GGA         GGA         CAG         GAC         TGA         AAA         CCT         TGC         CAA         GGA         CAG         TTC         TTC         TGC         TAG         CTC         TTC         TTC

FIGURE 1C

Serial No.: To Be Assigned

E.	<b>~</b> (1)	a. r.	10.5.	<b>-</b> 5.	r.	an 23
54 GCC	108 ACC T		216 CCT P	270 GTT V	324 TTT F	378 GGC G
GCT	GCC		TAC Y	GTC V	GAC D	TGT C
TAC	GCC			GTA V		
45 GTC	99 GCT A			261 AAA K		
AGC	CTG L	ACA T		GGA		1990 1990
900	CTG	TTC F	TTT F	GAA E	CTG L	ATT I
36 AAC	90 CTG L	144 GTT V	198 GGT G	252 CCC P	306 AAC N	360 CGC R
GGT GCA	TGC	CCT	GAA E	GTT V	GAC D	CAG Q
GGT	CTC	AGA (	AGT	ACA T	AGT S	299
27 GCG		135 GAG E			297 GAG E	351 AAT N
CGT	GCG	CCA P	ATT I	AAA K		GCC
505	TGG W	TCC	TYTT F	TGG W		CAT H
18 GGC	72 GCC A	126 CAG Q	180 GGA G	234 ACT T	288 ATA I	342 GGC G
299	AAC N	CAG Q	TCT	TGT C	TTC	AAT N
TGC	GCG <b>A</b>	CGG R	GAG E	AAA K	CGA R	TAC Y
990 ·	63 GGC G	117 TCG S	171 GGA G	225 AGC S	279 I'TC F	333 GTG V
TCT	AGG R	117 ; CTC TCG L S	ACT T	AAT N	AAT N	GAT D
5' CGC TGT	ATG M	CAG Q	CTT ACT (	CCA AAT P N	CTC	333 GTG GAT GTG V D V
5.						

# FIGURE2A

432	486	540	594	648	702	756
ATG	GCT	TCC	ACT	GAG	TTT	AGT
M	A	S	T	E	F	S
CAG	GCT	CCT	GTC	TTT	GTG	GAT
Q	A		V	F	V	D
GTG V	TCC	AGA R	GGA	AAG K	GCT	
423	477	531	585	639	693	747
ATG	TTC	GAC	GCA	TTA	GTG	TGT
M	F	D	A	L	V	C
ATG M	ATG M	CTT L	CCT	GAA E	TAT	TAT Y
AAG	GCC	CTC	TAC	ATA	GAT	AAG
K		L	Y	I	D	K
	468	522	576	630	684	738
	ATG	GGA	GAT	CTT	TAT	GGA
	M	G	D	L	Y	G
299	$\mathrm{TTC}$	GGA	CGG R	CAG	CGA R	ATT I
AGT S		TGT	GAC D	AAT	TGC	AGA R
405	459	513	567	621	675	729
TCC	AAT	TAT	CCA	AAG	TAC	AGA
S	N	Y	P	K	Y	R
GTG V			TGG W		AAC N	GCT A
CTT	GCT	GAT D	AAC N			
396	450	504	558	612	666	720
GCC	ACA	GGG	CCC	GTA	CGA	AAC
A	T	G	P	V	R	N
GGA G	AAC N				GAG E	GTC V
CCT	GCC	GAA	AAA	CAC	GTG	GAA
P		E	K	H	V	E
387	441	495	549	603	657	711
CGG	GAT	AAC	TTT	TGG	GAT	GGG
R	D	N	F	W	D	G
TTC	TYTT	CCA	TCT	GTG	TYTT	9
	F	P	S	V	F	9
ACT T	ATT I	GAA E	9 299	TGT	AAG K	AAT N

### FIGURE2E

Serial No.: To Be Assigned

810 TCA S	864 AAA K	918 ACG T	972 ACT T	.026 ACA T	.080 TAC Y	134 CTG L
TTA L	CCA P	ACC	999 9	1 ATC I	ATC I	1 AGG R
T'I'I F	AGG R	GTA V	ACG	GTT V	AAC N	GCC
801 CAG Q	855 TTC F	182 891 900 909 918 ICA GAA CAG CCT GTC ACC ACC ACG I E Q P V T T T F P V T T	963 CGG R	.017 ACT T	.071 ATC I	.125 AGT S
ATT I	ATA I	TTC	AGA R	ggc G	1 ATC I	1 ATG M
CTT L	TAC Y	ACA T	TGT C	GCC	TCG	AAC N
792 CTT L	846 CAC H	900 ACC T	954 AAG K	_008 TTA L	.062 GTC V	.116 AAG K
GAA E	GGT	ACC T	CAA Q	1 GTA V	ACA T	1 GGC G
AAT N	AT'T I	GTC V	CAA Q	TTT F	GCC	GCG
783 AGA R	837 T'T'T F	891 CCT P	945 TGT C	999 GAC D	.053 CAC H	.107 CAG Q
GAG E	9 9	CAG Q	TTG	AGT S	1 TTG L	cag Q
TCT	GAT D	GAA E	GCC	TCA	AGT S	ATT I
	$\omega$ $\omega$	8 A L	936 GTG V	990 TGT C	.044 GGG G	.098 GCG A
ATT I	ACT T	ACT T	ACC	TAT Y	1044 GAT GGG 7 D G S	1 TTG L
CCA	TTA L	ACA T	GCC	AAT N	CGC R	AAT N
765 GCG A	819 AGT S	873 CCT P	927 AAA K	981 GGC G	1035 ACT T	L089 GGA G
CCA CCT P P	GAC TTA D L	AAA CTG K L	TTA L	981 GAG GGC E G	ATC I	GAG E
CCA P	GAC	AAA K	927 GGT TTA AAA G L K	CTG L	1035 ACC ATC ACT T I T	1089 AAA GAG GGA K E G

### FIGURE2C

Serial No.: To Be Assigned

1188	ACT GTC GTC TGC AAG CAG TGC CCT CTC CTC AGA AGA GGT CTA AAT TAC ATT ATT T V V C K Q C P L L R R G L N Y I I	1197 1206 1215 1224 1233 1242 ATG GGC CAA GTA GGT GAA GGT GGG CGA GGC AAA ATC ATG CCA AAC AGC TTT ATC M G Q V G E D G R G K I M P N S F I	1251 1260 1269 1278 1287 1296 ATG ATG TTC AAG ACC AAG AAT CAG AAG CTC CTG GAT GCC TTA AAA AAT AAG CAA M M F K T K N Q K L L D A L K N K Q	1305 1314 1323 1332 1341 1350 TGT TAA CAG TGA ACT GTG TCC ATT TAA GCT GTA TTC TGC CAT TGC CTT TGA AAG C	1368 1377 1386 1395 1404 CTC TCA GTA GAA AAA ATA CTT ATA AAA TTA CAT ATT CTG AAA	1413 1422 1431 1440 1449 1458 GAG GAT TCC GAA AGA TGG GAC TGG TTG ACT CTT CAC ATG ATG GAG GTA TGA GGC	1467 1476 1485 1494 1503 1512 CTC CGA GAT AGC TGA AGG TTC TTT GCC TGC TGT CAG AGG AGC AGC TAT CTG
	TAC Y	AGC S	AAT N	CTT	ATT	GTA	AGC
1179	, AAT N	1233 A AAC A N S	1287 1 AAA K	1341 ' TGC	1395 \ CAT	1449 3 GAG	1503 3 AGC
	CTA	CCA	TTA L	CAT	TTA	ATG	AGG
	GGT G	ATG M	GCC A	TGC	AAA	ATG	CAG
1170	AGA R	1224 ATC I	1278 3 GAT D	1332 \ TTC	1386 1 ATA	1440 r CAC	1494 7 TGT
7	AGA R	AAA K	CTG	GTA	CTT	CTT	TGC
	CTC L	1990 1990	CTC L	GCT	ATA	ACT	$\mathcal{O}\mathcal{O}$
1161	CTC L	1215 3 CGA R	1269 ; AAG K	1323 ATT TAA	1377 1 AAA	1431 3 TTG	1485 TTT
-	CCT P	GGG G	CAG Q	1 ATT	1 AAA	1 TGG	1 TTC
	TGC	GAT D	AAT N	TCC	GAA	GAC	AAG
1152	CAG Q	1206 ' GAA E	1260 : AAG K	1314 . GTG	1368 GTA	1422 \ TGG	1476 \ GGG
-	AAG K	ogt G	ACC T	1 ACT	1 TCA	1 AGA	TGA
	TGC C	GTA V	AAG K	TGA	CTC	GAA	AGC
1143	GTC V	1197 CAA Q	1251 TTC F	1305 . CAG	1359 ' GTT	1413 TCC	1467 GAT
7	GTC V	ggc G	1 ATG M	1 TAA	1359 ATC TAT GTT	1 GAT	1 CGA
	ACT T	ATG M	ATG M	TGT C	ATC	GAG	CTC

### FIGURE 2D

Docket No.: PF-0479-2 DIV Inventors: Bandman et al. Title: HUMAN PROTEINASE MOLECULES

TCA AGC GTT	1620 . GAA TTG	1674 . GTG TTA	1728 GCG TTT	1782 AAA AAA	
TCA	TTA	ATA	CTT	AAA	
GTG	1611 ATT	1665 TTT	1719 ' TGT	1773 AAA	
AAA	1611 GAT ATT	1 ATA	1719 TCT TGT	1773 AAA AAA AAA	
CTA		GCA		AAA	
CCG ACT TAG TGC GGT GAT AGG AAG CTA AAA GTG	1602 CTG TAA AAG	1656 1665 AGA AGT GCA ATA TTT	1710 GTG TTA CAA	1764 TTA AAG GAA AAA	
AGG		1 AGA		1 AAG	
GAT	1593 TAT ACA TCT	1647 AAA GAT TTT	1701 TGC CCT GAG	TTA	
GGT	1593 ' ACA	1647 GAT	1701 : CCT	1755 TTT	
TGC			1 TGC	1 ATA	-
TAG	ATT	AAA	CTT	AAA	AT 3
ACT	1584 GAA GCG TTT	1638 AAG ATG TCA AAA	1692 TCA AGC CTT	1746 1755 CTT AAT AAA ATA TTT	1800 AAA AAA CGA AT 3'
900	່ອວອ	ATG	TCA		AAA
CTG	GAA	AAG	CCT	ATG	AAA
AAC	1575 : TTG	1629 GTG	1683 TCA	1737 . TCA	1791 AAA
ATT GGA AAC	1575 GAC AGC TTG	1629 AGT TGT GTG	1683 TTT GTT TCA	1737 TCT AAA TCA	1791 AAA AAA AAA
ATT	GAC	AGT	TTT	TCT	AAA

FIGURE 2E

56 CTY L	110 GTG V	164 CTC L	218 TGC C	272 TAC Y	326 GAC D	380 TGC C
CTT	AGG R	CAG Q	TCC	GAA E	TTC F	GCC
			GAG E			
	101 CTT L	155 CGG R	209 ACC T	263 GAT D	317 GTC V	371 AGC S
AAA K	TCC	GCA	TTC	TTG L	ACT T	ACT T
ATG M	GGA	CGG R	CAG Q	TAC Y	TTC F	TGC
38 ACA A	92 CAA Q	146 CTG L	200 ATC I	254 AAC N	308 AAC N	362 TAC Y
CTC	GCC	AAG K	ATG M	ATC I	CAG Q	GTG V
GGA	GAG E	AAG K	GAC D	CTC L	CCA P	TCT S
29 GTC	83 GGA G	137 AAG K	191 TTG L	245 CCC P	299 CCA P	353 CCC P
CTG	CTG L	CTC L	AAT N			
CTG	GAG E	TCC	CAT H	AAG K	299	TGG W
20 AAG	74 CTG L	128 CCG P	182 TCC S	236 GCC A	290 ATT I	344 CTC L
GAG	CTC L	CAT H	AAA K	AGT	TCC	AAC N
AGG	GTG V	AGG R	TGG W	CAG Q	ATC I,	TCC
11 GCA	65 CTG L	119 AGG R	173 TTC TGG AAA F W K	227 GAC D	281 ACT T	335 TCC S
999	CTG L	CTC L	GAG E	ATG M	9 ე99	ე ექ
GAG	TTG L	CCC	TCT	TCA	TTC	ACT T
5'CG GAG GGG						

# FIGURE3A

Docket No.: PF-0479-2 DIV Inventors: Bandman et al.

Title: HUMAN PROTEINASE MOLECULES

Serial No.: To Be Assigned

434	488	542	596	650	704	758
GGT	GCC	AGT	GGC	ATG	AAC	CAT
G	A	S	G	M	N	H
CCA P	GGA G			AAC N		
CAG	ATT	GGA	ATT	GAC	AGC	CAC
Q	I	G	I	D		H
425	479	533	587	641	695	749
AGC	ATC	TTT	GGA	TYT	ATG	GAC
S	I	F	G	F	M	D
TAC		CAG	GAT	GTA	TAC	TAC
Y		Q	D	V	Y	Y
ACA T				CCA P		
416	470	524	578	632	686	740
AGC	TTG	GGC	GAG	ACT	TCT	GGA
S	L	G	E	T	S	G
TCC	AGC S			GTG V		
	999 9	GTG V	GAT D	GGA	ATG M	ATT I
407		515	569	623	677	731
TCC		ACC	GTG	GGA	CCG	CTG
S		T	V	G	P	L
CCT				GTG V	${\rm TTG}_{\rm L}$	GAG E
CAG Q	TAT Y	GGA	ACC T	GCT A	GAC D	AGC
398	452	506	560	614	668	722
TTC	CAG	Gaa	CAG	TTG	GTG	GGG
F	Q	E	Q	L	V	G
AGG R	ATT I	GTG V			CTG L	GCC
AGC S	TCC	TCT S	CCA P	CCC	AAC N	GGT G
389	443	497	551	605	659	713
CAC	TCT TTC	GTC	GAG	TAC	CAG	GGT
H	S F	V	E	Y	Q	G
3 ACG C.	TCT	CAA	ACA	GGA	GCT	GAA
T H	S	Q	T	G		E
AAG K	CAA	GAC D	GTC V	CTG	ATG M	CCA P

### FIGURE 3E

812 ATT I	857 866 C ATG CCG GAT GTC M P D V	884 893 902 911 920 ATT AAC GGA GTC CCC TAT ACC CTC AGC CCA ACT GCC TAC ACC CTA I N G V P Y T L S P T A Y T L	974 GAC D	1028 CAG Q	1082 GTC V	1136 ATG
CAG Q	GAT D	ACC T	CTT L	CGA	GCA	AAT
TGG W	CCG P	TAC Y	GGA	ATT I	CCA P	TTG
803 TAC Y	857 ATG M	911 GCC A	965 CAA Q	1019 TTC F	L073 GCC A	127 ACC
GCT	GTC V	ACT T	TYYY F	GTC V	CTG L	CAG
CAA Q	AAC N	CCA P	ე ენე	GAT D	GGA G	TGA
794 AAG K	848 CTT L	902 AGC S	956 AGT S	.010 GGG G	1064 GTG V	.118 GTC
ACC T	AAC N	CTC L	AGC	1 CTG L	1 CGT R	CCT
GTC V	GCC	ACC T	TGC	ATC I	AAC N	CTG
785 CCA P	839 TGT C	893 TAT Y	947 TTC F	.001 TGG W	.055 AAT N	.109 TGC
GTC V	GAG	CCC P	CAG Q	1 CTC L	1 GGG G	1 CTG
TGG W	GTG V	GTC V	ATG M	CCC	CGT R	TGT
776 AAT N	830 GCT A	884 GGA G	938 GGA G	992 GGG G	.046 GAC D	.100 TTG
CTG L	TAT Y	AAC N	GAT D	GCT A	1 TYYT F	1100 GGG GCC TTG
AGC S	AAC	ATT			O P	_
767 GGG G	821 GAT D	875 ACC T	929 TTC F	983 CCT P	1037 TCA S	1091 GGA
TTC TCT F	GCA CTG A L	TTC	929 3 GAC TTC D F	983 CAC CCT H P	1 TAC Y	1091 TAA GGA
TTC	GCA	ACC T	CTG L	ATC I	1037 TTT TAC TCA F Y S	CCC

FIGURE3C

Serial No.: To Be Assigned

AAA AAG TTA TTT TCC AGA GAA TGT AGC	1244	1289 1298	1352	1397 1406	1460	1496 1505 1514	1568	1604 1613 1622
	AAT ACA CAC	ACA CTC CCA CCA	TT TTT GAT	TCC AAA CAT ATG CAC	CCC TGA CAA	TAC ACT GCC CAC TCT CTC	AT TAC ATC	CTT AAA TAT ACA ATC GGA ATT CAA GCA
1181 TCC AGA G	1235 CAT GAG		1343 GTA TTG ATT		1451 ACT CAG	1505 r GCC CAC 1	1550 1559 GAA GCA AAT TCC GAG CAT	1613 A ATC GGA A
TTT	GAA	TAC	I'I'I	ATC	TCC	GCI	AA	ACA
1172	1226	1280	1334	1388	1442		1550	1604
AAG TTA	CAA ACA	CAC ACA	TCA TAT	ATG AAA	TGC AAC		GAA GCA	AAA TAT
AAA	GAC	CTT	CAT	ATT	CTT	ATC	TCT	CTT
1163	121 <i>7</i>	1271	1325	1370 1379 1388	1433	1478 1487	1541	1595
TAC ACC TAC	AAT TAA	A CAC ACA	CTT ATA	AAA TIT TCA CAT TIG ATT ATG AAA ATC	AAA TCC	CGG CCA GGC CTG TTT ATC	3 GAT CAT TCT	F AAC ATC
TAC	TTG	ACA	TAC	TC?	AA.	99	CTC	TC
1154	1208	1262 1271 1280	1316 1325 1334	1370	1424	1478	1532	1586 1595
GGC ATT CTT	GGT TGC AAC	CAT ATA CAC ACA CAC ACA TAC	TGG AGG AAT TAC GTT ATA CAT TCA TAT TTT	CAA AAA TTT	TCA TGG TAT AAT	ACA CGG CCA	ATG CTG TAC CTG	ATA AAT ATT TCT AAC ATC
1145	1199	1253	1307	1361	1415	1469	1523	1577
TTA GGC TGG	TGT TTC CAG	ACA CAC ACA	CCG TCA TGA	GAA AAT	AAG CAG AGA	CCC ATC CAC	CAG CTC CAC	ATT TYG TCC
TTA	TGT	ACA	900	TAT	AAG	သသ	CAG	ATT

### FIGURE 3L

76 I'T	30 CT	84 IG	38 CT	92 IG	46 A.A	00 AG	54 4.A	
1676 TGT ATT	1730 GTC TCT	1784 GAG GTG	1838 AGA TCT	1892 TTC TTG	1946 TGT TAA	2000 GTT CAG	2054 AAA GAA	
GTT	TAA	၁၁၁	GTT	TAC	TAA	AAA	AAA	
1667 TGG ATT	1721 TGT CTG	1775 TGA AAT	1820 1829 TCC TAT AAA ATG GTA	1883 GCT GGG	1937 TAT TGG	1991 CAT TAC	2045 AAA GAG	
1766			ATG		TAT	CAT	AAA	
AGT	AAA	CGT	AAA	GGT	CTC	ATT	GAA	
1658 TTT TGT	1712 TAT TTG	1766 GTT GCT	1820 TAT	1874 CTA GGT	1928 GTG CCT	1982 TTA ATC	2036 AAA AAG AAA GAA	
TTT	1 TAT			1 CTA	1 GTG		2 AAG	
TGT	ATT	AAC	CTT	TTC	CTG	GCT	AAA	
1649 TTT GGC	1703 TAT TGC	1757 CAT TTG	1811 TGA ACT TAT	1865 AAA TAC	1919 ATA ATG	1973 TTC TTG	2018 2027 AAA AAA AAA GGA	
		CAT	ACT	AAA			AAA	_
ATG	ATA	GCA	TGA	CAA	CAG	GAG	AAA	G 3
1640 CCA CAA ATG	1694 AGG CCC	1748 AGT TTA	1802 GTT CTC	1856 TTG TGG	1910 AGG AGG	1964 GGT TTG	2018 AAA	2072 AGA GGG
				1 TTG	J AGG	1 GGT		
GTC	GCA	CAG	ATG	ATT	GTC	GTG	AAA	GAA
1631 ATT	1685 CAA	1739 CTA	1793 ' GAC	1847 CTG	1901 CCT	1955 TGG	2009	2063 AAG
1631 TCT CCC ATT	1685 AGG ATT CAA	1739 TTC CAT CTA	1793 TCA TTT GAC	1847 GGA GGT CTG	1901 TTG CAT CCT	1955 GAC TGC TGG	2009 CAT TTT AAA	2063 aaa aaa aag
TCT	AGG	TTC	TCA	GGA	TTG	GAC	CAT	AAA

FIGURE3E

пп	MFLVNSFLKGGGGGGGGGGGLGLGNVLG g164403
22	GLFGGGGRREGGGRNIGG IV 456855 GLISGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
42	GGIVNFISEAAAQYTPEPPTQQHFTSVE 456855 GGVISAISEAAA-QYNPEPPPRTHYSNIE 9164403
8 9	ASESEEVRRFRQQFTQLAGPDMEVGATDLM 456855 ANESEEVRQFRRLFAQLAGDDMEVSATELM 9164403
102	102 NILNKVLSKHKDLKTDGFSLDTCRSIVSVM 456855 120 NILNKVVTRHPDLKTDGFGIDTCRSMVAVM 0164403

FIGURE 4A

c	<b>1</b>		Ж		മ		٣
132 DSDTTGKLGFEEFKYLWNNIKKWQCVYKQY  456855	910440	162 DRDHSGSLGSSQLRGALQAAGFQLNEQLYQ 456855	g16440	192 MIVRRYANEDGDMDFNNFISCLVRLDAMFR 456855	g16440	456855	g164403
<b>&gt;</b>	<b>L</b> ,	a	S	R	R		
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132		162	180	192	210	222 AFKSLDRDRDGLIQVSIKEWLQLTMYS	240 AFKSLDKDGTGQIQVNIQEWLQLTMYS

FIGURE 4B

Н,	
<b>-</b>	MLPARLTSFLIGPFLLAMVLPLARIGOTPNYT 92589009
88	RPVFTCGGILTGESGFIGSEGFPGVYPPNS 947429
31	RPVFLCGGDVTGESGYVASEGFPNLYPPNK 92589009
83	KCTWKITVPEGKVVVLNFRFIDLESDNLCR 947429
61	KCIMTITVPEGQTUSLSFRVFDMELHPSCR 92589009
88	YDFVDVYNGHA - NGQRIGRFCGTFRPGALV 947429
91	YDALEWFAGSGTSGQRLGRFCGTFRPAPVW 92589009
117	SSGNKMMVQMIFDANTAGNGFMAMFSAAEP 947429
121	APGNQVTLRMTTDEGTGGRGFLLWYSGRAT 92589009
117	N T T T T T T T T T T T T T T T T T T T
151	
177	AGVTCVWHIVAPKNQLIELKFEKFDVERDM 947429
181	PGISCSWHIIAPSNQVIMLTFGKFDVEPDT 92589009

### FIGURE 5A

207 YCRYDYVAVFNGGEVNDARRIGKYCGDSPP 947429 211 YCRYDSVFNGAVSDDSKRLGKFCGDKAP g2589009
237 APIVSERNELLIQFLSDLSLTADGFIGHYI 947429 241 SPISSEGNELLVQFVSDLSVTADGFSASYR 92589009
APIVSERNELLIQFLSDLSLTADGFIGHYI SPISSEGNELLVQFVSDLSVTADGFSASYR E
A P I V S E R N E L L I Q F L S D L S L T A D G F I G H Y I S P I S E G N E L L V Q F V S D L S V T A D G F S A S Y R F L P R D A V E K E S A L S P G E D V Q R G P Q S R S D P K T G T G P K V K P P T K P K S Q P A E T P E A S P A T Q A T
APIVSERNELLIQFLSDLSLTADGFIGHYISPISSEGNELLVQFVSDLSVTADGFSASYR  F

FIGURE 5F